



2121

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/032,260
Source: OIPE
Date Processed by STIC: 2/26/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/032,260

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/032,260

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

pp 1-7

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: de Belle, Ian
 4 Adamson, Eileen
 5 Mercola, Dan
 7 <120> TITLE OF INVENTION: Isolation and Identification of Control Sequences and
 8 Genes Modulated by Transcription Factors
 10 <130> FILE REFERENCE: PS-00101.P.1
 12 <140> CURRENT APPLICATION NUMBER: US/10/032,260
 13 <141> CURRENT FILING DATE: 2001-12-20
 15 <160> NUMBER OF SEQ ID NOS: 27
 17 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

35 <210> SEQ ID NO: 3
 36 <211> LENGTH: 20
 37 <212> TYPE: PRT
 38 <213> ORGANISM: Homo sapiens
 40 <400> SEQUENCE: 3
 41 Cys Asp Asn Phe Ser Ala Tyr Gly Trp Cys Pro Leu Gly Pro Gln Cys
 E--> 42 1 5 5 10 10 15 15
 44 Pro Gln Ser His
 45 20
 47 <210> SEQ ID NO: 4
 48 <211> LENGTH: 31
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens
 52 <400> SEQUENCE: 4
 53 Ile Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg Arg Arg
 E--> 54 1 5 10 15
 56 Arg Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro Gly
 E--> 57 20 25 30
 59 <210> SEQ ID NO: 5
 60 <211> LENGTH: 13
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Homo sapiens
 64 <400> SEQUENCE: 5
 65 His Arg Ala Gly Phe Asp Ala Phe Met Thr Gly Tyr Val
 E--> 66 1 5 10
 221 <210> SEQ ID NO: 16
 222 <211> LENGTH: 234
 223 <212> TYPE: PRT
 224 <213> ORGANISM: Homo sapiens

misaligned amino
 acid numbers -
 see item 3 on
 Error Summary
 sheet-global
 error

same error

same

p. 2

RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/032,260

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

226 <400> SEQUENCE: 16
 227 Met Arg Asp His Ile Asp Tyr Arg Cys Cys Leu Pro Pro Ala Thr His
 E--> 228 1 5 10 15
 229 Arg Pro His Pro Thr Ser Ile Cys Asp Asn Phe Ser Ala Tyr Gly Trp
 E--> 230 20 25 30 *same*
 231 Cys Pro Leu Gly Pro Gln Cys Pro Gln Ser His Asp Ile Asp Pro Ile
 E--> 232 35 40 45
 233 Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg Arg Arg Arg
 E--> 234 50 55 60
 235 Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro Gly Thr Gln
 E--> 236 65 70 75 80
 237 Thr Ser Gly Glu Ala Lys Asp Gly Pro Pro Lys Lys Gln Val Cys Gly
 E--> 238 85 90 95
 239 Asp Ser Ile Lys Pro Glu Glu Thr Glu Gln Glu Val Ala Ala Asp Glu
 E--> 240 100 105 110
 241 Thr Arg Asn Leu Pro His Ser Lys Gln Gly Asn Lys Asn Asp Leu Glu
 E--> 242 115 120 125
 243 Met Gly Ile Lys Ala Ala Arg Pro Glu Ile Ala Asp Arg Ala Thr Ser
 E--> 244 130 135 140
 245 Glu Val Pro Gly Ser Gln Ala Ser Pro Asn Pro Val Pro Gly Gly Gly
 E--> 246 145 150 155 160
 247 Leu His Arg Ala Gly Phe Asp Ala Phe Met Thr Gly Tyr Val Met Ala
 E--> 248 165 170 175
 249 Tyr Val Glu Val Ser Gln Gly Pro Gln Pro Cys Ser Ser Gly Pro Trp
 E--> 250 180 185 190
 251 Leu Pro Glu Cys His Asn Lys Val Tyr Leu Ser Gly Lys Ala Val Pro
 E--> 252 195 200 205
 253 Leu Thr Val Ala Lys Ser Gln Phe Ser Arg Ser Ser Lys Ala His Asn
 E--> 254 210 215 220
 255 Gln Lys Met Lys Leu Thr Trp Gly Ser Ser
 E--> 256 225 230
 258 <210> SEQ ID NO: 17
 259 <211> LENGTH: 725 *724 shown*
 260 <212> TYPE: DNA
 261 <213> ORGANISM: Homo sapiens
 263 <400> SEQUENCE: 17
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 265 tctcccatgt ctactttctt ctacacagac acagcaacca tccgattttct caatcttttc 120
 266 cccaccttttc cccctttttct attccacaaa accgccattg tcatcatggg ccgtttctcaa 180
 267 tgagctgttg ggtgagatat tagaattcta ctacagaaac gaaatgaaaa gtctcccatg 240
 268 tctactttct ctacacaaga cacagcaaca tccgattttct caatcttttc cccaactttc 300
 E--> 269 cccctttttct antccacaan accgccattg tcatcatggg ncgtttctcaa tgagctgttg 360
 270 ggtgagatat tagaattctg ggctgggaat gagttcagcc tgggtggaatg tgaacctgca 420
 E--> 271 ncagtttggc atgaacgggc aaatgctgtg tancctccgg aaaggagcgc ttcctggaag 480
 E--> 272 ctggcgctg actttgtggg ngacatcctc cgggaaaang gttcactant tctaaagcgg 540
 E--> 273 gcggcaacgc ggtggggctc caattgcgcc taaantgngt ccgtattaca attcacnggg 600
 E--> 274 cggccgtttt anaagtctg nncggggaaa accnggggt anccaacttt atnccectgg 660
 E--> 275 nngaaanccc ccttncnca acnggggtna naaccnannn gggcncnccn ntttgccect 720
 E--> 276 cccaa 725 *724*

*see item 9 on Enol
 Summary
 sheet*

item 9

item 9

659

719 nos. off

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

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278 <210> SEQ ID NO: 18
279 <211> LENGTH: (619) 618 shown
280 <212> TYPE: DNA
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 18
284 agaagcttga attcgagcag agaagcttga attcgagcag aattggccca attttgcctt 60
285 ataccacttt ccaatacctt cacttggagt gacttacact gtggttaatt gcagttacaa 120
286 tgaagagatt aacatgggaa tgtcataata attgaatcta aagaagacat aatttcaaaa 180
287 taagagcttg agtaataata ccattgtgta acaatctgat ttccatccct cttatttttc 240
288 ctatattatg cagtttagtt ctttactatc atgtgtttca tgtttgttcg gttttaccaa 300
289 cacatcatta gtaaatgaa tgtaaggctt ctcatctctt ttgtatccta catctaaaag 360
290 attttagtcc ttagaatcct cttgaaatgt tctccattta aaatggagaa atagttcatg 420
E--> 291 ctctctcatc taagtangag ctaaaatcta aaaaattaat aaataaaata gtccatcctc 480
E--> 292 taataataat aatgaatact gaanttgtta antaataatt aatttttgag aaggggggtc 540
E--> 293 actaatgcg tccaagctgg agtgcaatgg cgtgatcact aanttctaaa ncggcgccaa 600
E--> 294 cgcggtggag ctccaantn (619) 618 (549) 549 numbering off
296 <210> SEQ ID NO: 19
297 <211> LENGTH: 716
298 <212> TYPE: DNA
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 19
E--> 302 gngtgggng nnnngggggg ggnntttng gnnccgntnt tctnaagtnt cnggggcctc 60
E--> 303 atnaaacagc gggccgagaa cgggnaana tgacaatgn ggttttggg aatagaaaag 120
304 ggggaaaggt ggggaaatga ttgagaaatc ggatggttc tgtgtctgtg tagaagaag 180
305 tagacatggg agacttttca ttttgttctg tgagtagaat tctgggctgg gaatgagttc 240
E--> 306 agcctggtga atgtgaacct gcaccagttt ggcataaacg gncagatgct gtgtaacctc 300
E--> 307 ggcaaggagc gcttcttga gctggcgctt gactttgtgg gcgacatcct ctggmacagg 360
E--> 308 ntccactagt tctagagcgg gcgccaccgc ggtggngctc caattegccc tanagtngt 420
E--> 309 cgtnttaciaa ttcactggcc gtcgttttac aacgctcgtga ctgggaaaac cctggngtta 480
E--> 310 cccaacttaa tcgccttgca gcanatcccc ctttcgncag ctggngtntt ancgangagg 540
E--> 311 nccgcaccgn ttgccntcc caanaagttg cgcagcctgn atggggantg ggancgncct 600
E--> 312 gtnnccggng cantaaagcg gnggggtgtg gtgngtange ncancgtggn cgnnnanant 660
E--> 313 gnnagnccct tangcngnn ccttcgnttc tcccttcctt cnnngnangt ngcggg 716
315 <210> SEQ ID NO: 20
316 <211> LENGTH: 619
317 <212> TYPE: DNA
318 <213> ORGANISM: Homo sapiens
320 <400> SEQUENCE: 20
321 agaagcttga attcgagcag agaagcttga attcgagcag aattggccca attttgcctt 60
322 ataccacttt ccaatacctt cacttggagt gacttacact gtggttaatt gcagttacaa 120
323 tgaagagatt aacatgggaa tgtcataata attgaatcta aagaagacat aatttcaaaa 180
324 taagagcttg agtaataata ccattgtgta acaatctgat ttccatccct cttatttttc 240
325 ctatattatg cagtttaagt tctttactat catgtgtttc atgtttgttc ggttttacc 300
E--> 326 acacatcatt agtaaatgga atgtangcct tctcatttct tttgtatcct acatctaaaa 360
327 gattttagtc tttagaatcc tcttgaaatg ttctccattt aaaatggaga aatagttcat 420
E--> 328 gctctctcat ctaantanga gctaaaatct aaaaaataa taaataaaat antccatcct 480
E--> 329 ctaataataa taatgaatac tgaanttgtg aataataatt aatttttgag aatgggggtc 540
E--> 330 actaatgtcg tccaanctgg agtgcaatgg cgtgatcact agttctaaac cggcgccaac 600
E--> 331 gcggtgggnc tccaattcc 619

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TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

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356 <210> SEQ ID NO: 22
357 <211> LENGTH: 419
358 <212> TYPE: DNA
359 <213> ORGANISM: Homo sapiens
361 <400> SEQUENCE: 22
362 acttgagtc ccaggagttcaa ggtgtagt agttgtgatt gcaacaacgc actccagcct 60
E--> 363 cgatgacaga gtgagaccct gtctgttaaa aaataataat aataatagat aatgggatan 120
E--> 364 gagtgtaaag aaagacagga tgccttcttag caaagttaca aaaaatatta atangtcttt 180
365 gtcacaata tatgttttgc tatgagctga gaagagaaaa tgaaaaagtg aaaataagat 240
E--> 366 ttctcaaggt acaactttga tgcagttcan gtcaaaccta ngtaagattt tgtttganag 300
367 tttgggaaat aaccattgtg gcaaggctgg aatgcaaate gattttttgc tgttacagaa 360
368 acagttaaag aatttatggg attttatatt aatttagtta gctttttatg aggagaatt 419
387 <210> SEQ ID NO: 24
388 <211> LENGTH: 584
389 <212> TYPE: DNA
390 <213> ORGANISM: Homo sapiens
392 <400> SEQUENCE: 24
393 agagcagtc ccagtatatata catacatata caagctacaa gctgcatatg taattttaaa 60
394 ttttctaata accacattta aaaaggtaaa aagaaactgt tgaaataaat tttaatatct 120
395 ttcatgaac ccaatatatg caaaatacta tcatttcaat tataaccaa ttaaaattaa 180
396 ggagatattt tacaattttc atattaacgt ttccaattct ggtgtgaatt ttacactcac 240
397 cgaacatctc aattctgaca agtcatttt taagtgctca acagctacgt gaggatagtg 300
E--> 398 gctattatgt cacaaatgc agctctangg atgaggacag ttacagaag atacttgagg 360
E--> 399 atacaggagc aagttaaatg gcagtttaag aaagcaaate cangatgtg gaaactccac 420
E--> 400 agaatanatg acctggtttc tcccttcaat catccctcca aaatagaat caatggcaga 480
E--> 401 aagaaaaaag anggaggctg ttgtancata aaatacttag ggacatacaa taaaacagt 540
E--> 402 gtagggtttt gttgaanccg attcactaca atgattcaca antt 584
404 <210> SEQ ID NO: 25
405 <211> LENGTH: 678
406 <212> TYPE: DNA
407 <213> ORGANISM: Homo sapiens
409 <400> SEQUENCE: 25
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E--> 411 ataagctana tatcggaattc ctgcagcccg ggggatctga tggttttata aaggggagtt 120
E--> 412 gcctgcgaa agctctctct tacctgccc catgtaagac cggactttgc tcctcattag 180
E--> 413 gtcaccctag ccatgtggaa ctgtgagtc attaaacctc ttctctttat aaattatgca 240
E--> 414 gtctcggata tgtctttatt agcaagggtg aaatgaacta atacaagggt cacgtggtaa 300
E--> 415 atatatttaa tattaaaaaa aaatcttcca aactattttc cagagtgtct gtacctttt 360
E--> 416 acatttccat gagcaacgta tgagtgattt agtttctttg acagcatttg gtatagttac 420
E--> 417 tattttttat ttagttgtt ctcatcctgg acttaatttg aattttccca atgatgagtg 480
418 atgttgaaaa ttttcttct gcttacttgt catctggata ttctcgtcaa taaaatgtct 540
E--> 419 cttantatcn ttgcccatt ttcaantgga ttctttttgt gttttatcat tgaattttta 600
E--> 420 gaattcttcn atttatagat atgaattaca gatanaatca tagatattat agatanatat 660
E--> 421 gagttatggt tcacnatt 678
423 <210> SEQ ID NO: 26
424 <211> LENGTH: 509
425 <212> TYPE: PRT
426 <213> ORGANISM: Homo sapiens
428 <400> SEQUENCE: 26

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RAW SEQUENCE LISTING

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Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

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      429 Met Ala Ala Asp Ser Asp Asp Gly Ala Val Ser Ala Pro Ala Ala Ser
E--> 430      1              5              10              15
      431 Asp Gly Gly Val Ser Lys Ser Thr Thr Ser Gly Glu Glu Leu Val Val
E--> 432              20              25              30
      433 Gln Val Pro Val Val Asp Val Gln Ser Asn Asn Phe Lys Glu Met Trp
E--> 434              35              40              45
      435 Pro Ser Leu Leu Ala Ile Lys Thr Ala Asn Phe Val Ala Val Asp Thr
E--> 436              50              55              60
      437 Glu Leu Ser Gly Leu Gly Asp Arg Lys Ser Leu Leu Asn Gln Cys Ile
E--> 438 65              70              75              80
      439 Glu Glu Arg Tyr Lys Ala Val Cys His Ala Ala Arg Thr Arg Ser Ile
E--> 440              85              90              95
      441 Leu Ser Leu Gly Leu Ala Cys Phe Lys Arg Gln Pro Asp Lys Gly Glu
E--> 442              100             105             110
      443 His Ser Tyr Leu Ala Gln Val Phe Asn Leu Thr Leu Leu Cys Met Glu
E--> 444              115             120             125
      445 Glu Tyr Val Ile Glu Pro Lys Ser Val Gln Phe Leu Ile Gln His Gly
E--> 446              130             135             140
      447 Phe Asn Phe Asn Gln Gln Tyr Ala Gln Gly Ile Pro Tyr His Lys Gly
E--> 448 145             150             155             160
      449 Asn Asp Lys Gly Asp Glu Ser Gln Ser Gln Ser Val Arg Thr Leu Phe
E--> 450              165             170             175
      451 Leu Glu Leu Ile Arg Ala Arg Arg Pro Leu Val Leu His Asn Gly Leu
E--> 452              180             185             190
      453 Ile Asp Leu Val Phe Leu Tyr Gln Asn Phe Tyr Ala His Leu Pro Glu
E--> 454              195             200             205
      455 Ser Leu Gly Thr Phe Thr Ala Asp Leu Cys Glu Met Phe Pro Ala Gly
E--> 456              210             215             220
      457 Ile Tyr Asp Thr Lys Tyr Ala Ala Glu Phe His Ala Arg Phe Val Ala
E--> 458 225             230             235             240
      459 Ser Tyr Leu Glu Tyr Ala Phe Arg Lys Cys Glu Arg Glu Asn Gly Lys
E--> 460              245             250             255
      461 Gln Arg Ala Ala Gly Ser Pro His Leu Thr Leu Glu Phe Cys Asn Tyr
E--> 462              260             265             270
      463 Pro Ser Ser Met Arg Asp His Ile Asp Tyr Arg Cys Cys Leu Pro Pro
E--> 464              275             280             285
      465 Ala Thr His Arg Pro His Pro Thr Ser Ile Cys Asp Asn Phe Ser Ala
E--> 466              290             295             300
      467 Tyr Gly Trp Cys Pro Leu Gly Pro Gln Cys Pro Gln Ser His Asp Ile
E--> 468 305             310             315             320
      469 Asp Leu Ile Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg
E--> 470              325             330             335
      471 Arg Arg Arg Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro
E--> 472              340             345             350
      473 Gly Thr Gln Thr Ser Gly Glu Ala Lys Asp Gly Pro Pro Lys Lys Gln
E--> 474              355             360             365
      475 Val Cys Gly Asp Ser Ile Lys Pro Glu Glu Thr Glu Gln Glu Val Ala
E--> 476              370             375             380
      477 Ala Asp Glu Thr Arg Asn Leu Pro His Ser Lys Gln Gly Asn Lys Asn

```

*misaligned
amino acid nos.*

*see
item 3*

on Enol

*Summary
Sheet*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

E--> 478 385 390 395 400
 479 Asp Leu Glu Met Gly Ile Lys Ala Ala Arg Pro Glu Ile Ala Asp Arg
 E--> 480 405 410 415
 481 Ala Thr Ser Glu Val Pro Gly Ser Gln Ala Ser Pro Asn Pro Val Pro
 E--> 482 420 425 430
 483 Gly Gly Gly Leu His Arg Ala Gly Phe Asp Ala Phe Met Thr Gly Tyr
 E--> 484 435 440 445
 485 Val Met Ala Tyr Val Glu Val Ser Gln Gly Pro Gln Pro Cys Ser Ser
 E--> 486 450 455 460
 487 Gly Pro Trp Leu Pro Glu Cys His Asn Lys Val Tyr Leu Ser Gly Lys
 E--> 488 465 470 475 480
 489 Ala Val Pro Leu Thr Val Ala Lys Ser Gln Phe Ser Arg Ser Ser Lys
 E--> 490 485 490 495
 491 Ala His Asn Gln Lys Met Lys Leu Thr Trp Gly Ser Ser
 E--> 492 500 505

*same
error*

495 <210> SEQ ID NO: 27

496 <211> LENGTH: (3938) 3935 (P.7)

497 <212> TYPE: DNA

498 <213> ORGANISM: Homo sapiens

500 <400> SEQUENCE: 27

501 agcttatatt ctaatgggga cagaaaagga ataatgaaca taagtaaatt ccataagatg 60
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 503 gccaaggtgg ggtttaatgt tgcaatttta aagactgtgg tcaaggtaga cccaaagcat 180
 504 tctaagttag tgcaaaggcc ccaaggaggg tgctgtggtat gtctgtggta cagtaagtag 240
 505 gtcaatgtgg ttagaatgga atgagatggg actgagtggg agaagaggtc agagaagtaa 300
 506 accagatgag gtggggagag gagggtcaca aagtacctta taggccattg gagggatttg 360
 507 gctgccacac ccttgcctctt agaaggcagt cctcttacta cagccttgca ggtccagtga 420
 508 tccggggcacc atccgcctca tcccctcact atgctctagc caaggttgac tgaatttagt 480
 509 tgcttaaaaa cctcaagtgt gtctgcccac cttggggcct cacacaatcc atttcctctg 540
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 511 tccaaatcag gtccccctcat cttatcctat cacatatttc tgccctgtag ctcttaccta 660
 512 atgtaatttt acattacttt gattctttcc atcagtgtgt acttcttgaa tttgactgta 720
 513 aaaaacgact tgagtgaag gactgattct cttgttgatt ggtgtgtgtc caaagtcagt 780
 514 gccaggtaaa ctgtacacaa tagatacctg ttaaatgaat taatgggatg ggggatagtc 840
 515 aaaagagttt ccttttttta ggataggaga aatccaaaga gtttttttat ttttgttttt 900
 516 tttttgtttg tttgttttgt ttttagagac agtgtgtccc tcactttgct gctctgccac 960
 517 tcaggctgga gtgcaataag aacatggctc actgcagcct cgacctcctg ggtcagacc 1020
 518 atcctctcac ctcagcctcc tgtagctggg actacaggtg cgcaccacca tgcccaacta 1080
 519 atttttaatt ttctttttgt agagacaagg ttctactatg ttgccaggc tagtcttgaa 1140
 520 ctcttagggg caagcgatcc tcccaccttg gcctcctaag atgattacag gccataagcc 1200
 521 actgcgcccg gcccaagcag ttctgaataa tgatgaaatg ggctcagttg agagaagctg 1260
 522 aagattaact ataaacaatg agtaacaaag gagcactgga aggcagaggt ggatgggaat 1320
 523 cgtagtgttt acggaggggac tagtctccaa taggaatttt tttttttttt ttttttttga 1380
 524 gacggagttt cgctcttggt gcctaggctg aagtgcaaaa tggcgtgatc tcggctcacc 1440
 525 gcaacctctg cctcccaggt tcaagcgatt ctccctgctc agcctcccaa gtagtgggat 1500
 526 tacaggcgcc cgcaccatac ccagctaatt tttttgtac ttttagtaga gacggggttt 1560
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 528 tcccaaagtg ctgggattac aggcgtgagc caccgcgcc ggctaggaa cctctttcaa 1680
 529 attcaatcac cctctaggtc gactataccg cctagctgct tcacaatttg tcccttctc 1740

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

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530 gccatccata ctgccagcct taattcaagt tcacattatc acttgattgg attattacaa 1800
531 aagcttccct accaatcggt cgtctttaca ccctgggcag cctcctccga tggcccaactc 1860
532 ccgcctcttt tcactttctg gagatcactg agctctccat cctctctggg aattttaccga 1920
533 tgcccagaac gcccttcttt cccccacag accctctcct agtctaactc ctgggcgtgc 1980
E--> 534 ttttaagctca gctcaggca gcgtcacctt ctctggaaag cccaaaccca gccaccccaac 2040
E--> 535 taccgcgtac ccgcggccca cgtgatgaa gacagcagaa cacggaggcc ccgcgttccc 2100
E--> 536 gccgcgagag caggagagaa agattacctc ccgcgagctc tagcgcgccc ggctttccgg 2160
E--> 537 cgcactccag ggggcgtggc tcgggtccac ccgggctgcg agccggcagc acaggccaat 2220
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E--> 539 gttcgaccca tcggcgaccc gacggcgaga ccccgcccca tccccgactg cctgaaccgc 2340
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E--> 544 atttcgtggc tgtggacacg gagctgagtg ggcttgggga caggaagagt ttgctgaacc 2640
E--> 545 agtgcatgga ggaacgttac aaggccgtgt gtcagtctgc caggaccctt tctatccttt 2700
E--> 546 ccctgggcct cgcctgcttc aagcggcagc cagacaaggg tgaacattcc tatctggctc 2760
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E--> 548 agttcctgat acagcatggc ttcaacttca accagcagta tgcccaaggc atccccctacc 2880
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E--> 551 tgtaccagaa cttctatgca cacctccctg agagtctggg aaccttcacc gctgacctgt 3060
E--> 552 gtgagatgtt cccagcagge atttatgaca ccaaatatgc tgetgagttt catgcccgtt 3120
E--> 553 tcgtggcctc ctacttagaa tatgccttcc ggaaatgtga acgggaaaat ggggaagcagc 3180
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E--> 555 gaccatattg attaccgctg ctgcctgccc ccagcaaccc accgtcctca tcccaccagc 3300
E--> 556 atctgtgaca acttctcgge ttatggctgg tgccccctgg gaccacagtg tctcagttct 3360
E--> 557 cacgatattg accttatcat tgacactgat gaggtgcgg cagaggacaa gcggcgacgg 3420
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E--> 561 acaaaaatga cttagagatg gggattaagg cagcaaggcc tgaaatagct gatagagcta 3660
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E--> 565 gtggcaaagc tgtacccctc acagtggcca agagccagtt ctctcgttcc tccaaagccc 3900
E--> 566 acaatcagaa gatgaagctc acttggggca gtagctga 3938
E--> 569

```

1
Delete

2039
↓
numbering
off

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:43

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
 L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:42 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 ✓
 L:54 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4 ✓
 M:332 Repeated in SeqNo=4
 L:66 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5 ✓
 L:152 M:283 W: Missing Blank Line separator, <400> field identifier
 L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
 L:228 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16 ✓
 M:332 Repeated in SeqNo=16
 L:264 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17 ✓
 M:340 Repeated in SeqNo=17
 L:274 M:254 E: No. of Bases conflict, LENGTH:Input:660 Counted:659 SEQ:17 ✓
 M:254 Repeated in SeqNo=17
 L:276 M:252 E: No. of Seq. differs, <211>LENGTH:Input:725 Found:724 SEQ:17 ✓
 L:291 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18 ✓
 M:340 Repeated in SeqNo=18
 L:293 M:254 E: No. of Bases conflict, LENGTH:Input:600 Counted:599 SEQ:18 ✓
 M:254 Repeated in SeqNo=18
 L:294 M:252 E: No. of Seq. differs, <211>LENGTH:Input:619 Found:618 SEQ:18 ✓
 L:302 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19 ✓
 M:340 Repeated in SeqNo=19
 L:326 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20 ✓
 M:340 Repeated in SeqNo=20
 L:363 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22 ✓
 M:340 Repeated in SeqNo=22
 L:398 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24 ✓
 M:340 Repeated in SeqNo=24
 L:410 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25 ✓
 M:340 Repeated in SeqNo=25
 L:411 M:254 E: No. of Bases conflict, LENGTH:Input:120 Counted:121 SEQ:25
 M:254 Repeated in SeqNo=25
 L:430 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
 M:332 Repeated in SeqNo=26

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:43

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

L:534 M:254 E: No. of Bases conflict, LENGTH:Input:2040 Counted:2039 SEQ:27
M:254 Repeated in SeqNo=27
L:569 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3938 Found:3935 SEQ:27